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DT Pate LA Engl FAN.CNT 1 SO PA CIO PI PRAI OS AB => dup rem PROCESSING F S G AN DN TI <u>₽</u> PH **"** ₽ <u>^</u> s 19 s 16 s 15 d 110 bib ab 1-2 English The present invention provides binding moieties for fibrin which have a variety of uses wherever detecting, isolating or localizing fibrin, and particularly fibrin as opposed to fibringen, is advantageous. Particularly disclosed are synthetic, isolated polypeptides capable of binding fibrin and recognizing the form of polymed, fibrin found in thrombi. In addn., the polypeptides have a slow dissoon, rate from fibrin, which improves their ability to form a contrast image at the site of a fibrin clot, making the disclosed binding moieties particularly WO 2002055544 ***Fibrin*** ***binding*** moieties useful as imaging agents Wescott, Charles R.; Beltzer, James P.; Sato, Aaron K. ANSWER 2 OF 2 CAPLUS COPYRIGHT 2004 ACS 2002:539700 CAPLUS MARPAT 139:138721 US 2003143158 US 2001-34974 PATENT NO. English U.S. Pat. Appl. Publ., 41 pp. CODEN: USXXCO Wescott, Charles R.; Beltzer, James ANSWER 1 OF 2 CAPLUS COPYRIGHT 2004 ACS on STN PCT Int. Appl., 89 pp. CODEN: PIXXD2 137:90279 useful as imaging agents for thrombi. Patent PATENT NO. Patent Dyax Corp., USA 2003:590577 CAPLUS ***Fibrin*** and fibrin (w) bind? 2 L9 AND FIBRIN (W) BIND? 9 18
COMPLETED FOR 18
249 DUP REM 18 (47 DUPLICATES REMOVED) 17 296 £6 217 5 OR. L7 KIND A1 8 ***binding*** 20030731 DATE 20020718 DATE moieties useful as imaging agents s P.; Sato, Aaron K. US 2001-34974 WO 2001-US49534 APPLICATION NO. APPLICATION NO. 8 NIS DATE 20011221 DATE 20011221 - Fire a street

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R: AT, BE, C IE, SI, L PRAI US 2000-747403 WO 2001-US49534 OS MARPAT 137:90279 110 127 148 149 140 5455 II V B & Ω The present invention provides binding moieties for fibrin which have a variety of uses wherever detecting, isolating or localizing fibrin, and particularly fibrin as opposed to fibrinogen, is advantageous.

Particularly disclosed are synthetic, isolated polypeptides capable of binding fibrin and recognizing the form of polymd. Fibrin found in thrombi. In addn, the polypeptides have a slow dissoon, rate from fibrin, which improves their ability to form a contrast image at the site of a fibrin clot, making the disclosed binding moieties particularly useful as imaging agents for thrombi. Among examples provided are: screening of phage display libraries using the sol, fibrin-derived polypeptide DD(E) as fibrin target, and scintigraphic imaging of clots in rabbits using 9pmC-clabeled epotides. his Ę ĕ rabbits (FILE 'HOME' ENTERED AT 20:02:30 ON 22 JUN 2004) R: AT, W: AE, AC RW: # 5 E G E using 99mTc-labeled peptides. , KE, IS, MW, MZ, DK, ES, FI, FR, CF, CG, CI, CM, A2 20031001, CH, DE, DK, ES, LT, LV, FI, RO, A 20001223 5,8,5,5,6,5 S S T I C A NN, ξĘ, es, es IS, PAZ, GN, C СК, В DZ, JP, MK, SI, ZM, EP 2001-997103 GR, Ħ, ¥2, % % E & 22 JUN MR, 'n, NE NE Ĭ, A H S K B B AT, PT, SN, 1221 , MO SE, 848486 1 6 3 5 3 4 5 L 무급통단 2 1 H F P 9

ů o 19 FILE 'REGISTRY' ENTERED AT 20:03:02 ON 22 JUN 2004

0 S C[PRNDQGESTW] [ANDQEGILMEPSTWYY] [EGKSY] [PDENQEGKSTW] [RGW] [LIKM 0 S CPCKGGTLC

0 S WKFCDGEPWLFCWDG

159 S C[PNQST] [ANDQEGILMEPSTWYY] [ES] [PDENQSTY] W[LIMNQSTV] [FWY] / SQSP 406 S L1/SQSP FILE 'BIOSIS, CAPLUS' ENTERED AT 20:33:24 ON
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libraries generated from various plants, including Zea mays, Glycine max, Arabidopsis thaliana, Lycopersicon esculentum, Oryza sativa, Triticum aesticum, Euglena gracilis, Chlorella vulgaris, Schizochytrium aggregatum, Brassica napus, Gossypium hirsutum, Cucumis sativis, Iilium asiatic, ANSWER 1 OF 249 CAPIUS COPYRIGHT 2004 ACS on STN DUPLICATE 1
This invention provides 36,564 polynucleotide sequences isolated from CDVA

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transgenic plants having improved biol, properties are identified from their FunCAT annotations. [This abstr. record is one of 19 records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.]. porrum. The open reading frame in each polynucleotide sequence is identified by a combination of predictive and homol.-based methods. Functions of polypeptides encoded by the polynucleotides sequences are detd. using a hierarchical classification tool, termed FuncAT, for Functional Categories Annotation Tool. Sequences useful for producing Sorghum bicolor, Chlorella sorokiniana, Cuphea pulcherrima, and Allium

AB E polynucleotide sequence is identified by a combination of predictive and homol. based methods. Functions of polypeptides encoded by the polynucleotides sequences are detd. using a hierarchical classification tool, termed funcAI, for Functional Categories Annotation Tool. Sequence useful for producing transgenic plants having improved biol. properties are identified from their FunCAI annotations. [This abstr. record is one of 72 records for this document necessitated by the large no. of index entries required to fully index the document and publication system ANSWER 2 OF 249 CAPIUS COPYRIGHT 2004 ACS on STN DUPLICATE 2
This invention provides 142,842 polynucleotide sequences isolated from a cDNA library generated from Glycine max. The open reading frame in each constraints.]. [This abstr. record is one Sequences

AB 159

biol. function of a Drosophila gene are provided, including various methods for the functional modification (e.g., overexpression, underexpression, mutation, knock-out) of one gene, or of two or more genes simultaneously. (This abstr. record is one of sixteen records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.). acid sequences of the encoded proteins, and derivs. (e.g., fragments) and analogs thereof. Special emphasis is given to NAA sequences encoding G protein-coupled receptors and chitin synthetase. The invention further relates to fragments (and derivs. and analogs thereof) of proteins which comprise one or more domains of a Drosophila protein. Antibodies to Drosophila proteins, and derivs. and analogs thereof, are also provided. Also provided herein are vectors and host cells comprising such nucleic acids. Methods of prodn. of a Drosophila protein (e.g., by recombination means), and derivs. and analogs thereof, are provided. Chimeric means), and derivs. and analogs thereof, are provided. Chimeric polypeptide mols. comprising polypeptides of the invention fused to heterologous polypeptide sequences are provided. Methods to identif adult heads of Drosophila melanogaster. Drosophila ESTs and sequence contigs derived from ESTs are useful as tools for retrieval of full-length protein coding sequences, for proteomic anal., for use in microarrays and ANSWER 3 OF 249 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 3
The present invention relates to Drosophila genes and methods for their
use. A library of 31,629 expressed sequence tags and contig sequences are
provided from tissues of mixed-stage embryos (0-20 h), imaginal disks, and gene expression anal., and for identification of pesticide targets the invention provides nucleotide sequences of Drosophila genes, amino Methods to identify the Thus,

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ANSWER 4 OF 249 CAPLUS COPYRIGHT 2004 ACS on STN
The statistical anal. described and claimed is a predictive statistical tree model that overcomes several problems obsd. in prior statistical models end regression analyses, while ensuring greater accuracy and predictive capabilities. Although the claimed use of the predictive statistical tree model described herein is directed to the prediction o to the prediction of a

AB 45

predictive anal. then uses these metagenes in a Bayesian classification tree anal. This generates multiple recursive partitions of the sample into subgroups (the 'leaves' of the classification tree), and assocs Bayesian predictive probabilities of outcomes with each subgroup. Overall predictions for an individual sample are then generated by averaging predictions, with appropriate wts., across many such tree models. The model includes the use of iterative out-of-sample, cross-validation predictions leaving each sample out of the data set one at a time, refitting the model from the remaining samples and using it to predict the hold-out case. This rigorously tests the predictive value of a model and the proposition of the data set one at the set of the sample out of the data set one at a time, refitting the model from the remaining samples and using it to predict the hold-out case. This rigorously tests the predictive value of a model and the proposition of the sample o to reduce noise, applies kmeans correlation-based clustering targeting a large no. of clusters, and then uses singular value decompos. (SVD) to ext. the single dominant factor (principal component) from each cluster. This generates a statistically significant no. of cluster-derived singular factors, that are referred to as metagenes, that characterize multiple applications including the prediction of disease states, susceptibility of disease states or any other biol. state of interest, as well as other applicable non-biol. states of interest. This model first screens genes patterns of expression of the genes across samples. The strategy aims to ext. multiple such patterns while reducing dimension and smoothing out gene-specific noise through the aggregation within clusters. Formal: disease in individuals, the claimed model can be used for a variety of they arise is the major goal.

ANSWER 5 OF 249 CAPLUS COPYRIGHT 2004 ACS on STN
The invention provides 1231 novel cDNAs isolated from human tissues, and
their encoded polypeptides, related nucleic acid and polypeptide compns.,
and related modulators, such as antibodies and small mol. modulators. The
invention also provides methods to make and use these polymucleotides,
polypeptides, related compns., and modulators. These methods include
diagnostic, prophylatetic, and therapeutic applications. The compns. and
methods of the invention are useful in treating proliferative disorders,
e.g., cancers, and inflammatory, immune, bacterial, and viral disorders.

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AB The invention relates to plant transcription factor polypeptides, polynucleotides that encode them, homologs from a variety of plant species, and mechads of using the polynucleotides and polypeptides to produce transgenic plants having advantageous properties compared to a ref. plant. The polynucleotides of the invention encode polypeptides that are members of well-known transcription factor families that are involved in cell differentiation and proliferation and the regulation of growth. Exemplary polynucleotides were identified in the Arabidopsis thaliana GenBank database using publicly available sequence anal. programs and parameters. Sequences initially identified were then further characterized to identify sequences comprising specified sequence strings corresponding to sequence motifs present in families of known transcription factors; polynucleotide sequences meeting such criteria were confirmed as transcription factors. Addnl. polynucleotides were identified by screening Arabidopsis thaliana and/or other plant cDN; libraries with probes corresponding to known transcription factors under libraries with probes corresponding to known transcription factors under low stringency hybridization conditions, and full-length coding sequences were subsequently recovered by the rapid amplification of cDNA ends (RACE) procedure. Arabidopsis plants were transformed with Arrobacterium procedure. Arabidopsis plants were transformed with Agrobacterium ${\mathbb R}^2$ tumefaciens with expression vector ${\mathbb T}{\mathbb F}$ gene knockouts or overexpression phenotypes. Sequence information related to these - - Byrither sk

polynucleotides and polypeptides can also be used in bioinformatic search methods and is also disclosed.

AH E

searched and interesting EST sequences identified by GEPIS (gene expression profiling in silico), a bioinformatics tool that characterizes genes of interest for new cancer therapeutic targets. Using this type of screening bioinformatics, various tumor-assoca. antigenic target (TAT) proteins (and their encoding nucleic acid mols). Were identified as being significantly overexpressed in particular type of cancer or certain ANSWER 7 OF 249 CAPLUS COPYRIGHT 2004 ACS on STU
The present invention provides a large no. of specific cDNA sequences
which are upregulated in certain tumor tissues as compared to their normal
tissue counterparts and therefore useful for the diagnosis and treatment
of tumor in mammals. An expressed sequence tag (EST) DNA database was publication system constraints.]. cancers as compared to other cancers and/or normal non-cancerous tissues. [This abstr. record is one of two records for this document necessitated by the large no. of index entries required to fully index the document and

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AB The present invention provides novel genes and proteins for diagnosing ovarian cancer and/or a likelihood for survival, or recurrence of disease, wherein the expression of the genes and proteins is up-regulated or down-regulated or assocd. With the occurrence or recurrence of a specific scanner sub-type. The ovarian cancer respection profiling of patients with ovarian cancer using customized Affymetrix GeneChip microarrays that comprise 58,618 oligonuclectide probe sets for anal. of 46,000 gene clusters, representing >90% of the predicted expressed genome. Validation of gene expression profiling was achieved using quant. RT-PCR. Using these methods, 284 up-regulated transcripts and 186 down-regulated transcripts were identified in subjects suffering specifically from serous, endometrioid, muchous or clear-cell ovarian cancer, or non-invasive (borderline) ovarian cancers of any phenotype, and subjects that suffered from recurrences of ovarian cancer in the medium term. The gene expression profiles are useful in diagnosis and prognosis of ovarian cancer, monitoring the efficacy of therapeutic treatments, and in the manuf. of medicants to treat ovarian

AB

ANSWER 9 OF 249 CAPLUS COPYRIGHT 2004 ACS on STN
The present invention relates to 123 novel human secreted proteins and isolated nucleic acids conty, the coding regions of the genes encoding such proteins. Tissue distribution, sequence homologies, and preferred epitope sites are provided for the secreted proteins, as well as chromosomal mapping of some of the genes. Also provided are vectors, host cells, antibodies, and recombinant methods for producing human secreted cells, antibodies, insect, and mammalian cells. The invention further proteins in bacterial, insect, and mammalian cells. The invention furth relates to diagnostic and therapeutic methods useful for diagnostic and treating disorders related to these novel human secreted proteins. High-throughput screening assays are also provided for various putative activities of the secreted proteins.

₽ ₽ 19 ANSWER 10 OF 249 CAPIUS COPYRIGHT 2004 ACS on SIN

The present invention provides novel nucleic acids and polypeptides encoded thereby that are highly duplicated and overexpressed in squamous cell carcinomas of a variety of tissues. Antibodies specific for binding

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ANSWER 81 OF 1990:211787

92 CAPLUS CAPLUS

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the novel polypeptides are also provided. The invention further discloses several assays for gene duplication and overexpression of the novel gene and excessive prodn. of the novel polypeptide in a sample. These assays permit assessing copy no. in a sample from a subject, and contribute to the diagnosis, prognosis and development of therapeutic strategy for a pathol. such as squamous cell carcinoma in a subject.

853 SO SO **∥** II V 11 1 110 110 110 ۵ s 19 d his FILE 'BIOSIS, CAPLUS' ENTERED AT 20:33:24 ON 22 JUN 2004 103 S L4 217 S L5 296 S L6 OR L7 249 DUP REM L8 (47 DUPLICATES REMOVED) 2 S L9 AND FIBRIN (W) BIND? gamma. gene and consists of 5 exons. Three single nucleotide differences with the cDNA sequence were obsd., but they do not change the amino acids encoded. The majority of the primary translation product (emino acids 153-625) is encoded in one large exon which also contains the tandem repeats unique to the A.alpha. chain. Another unique feature of this gene is that it contains a segment of 100 residues in intron C that are exclusively pyrimidines and >70% T residues. The sequences of the B.beta. and .gamma. chain genes (E.W. Davie et al., 1983, 1985) are also hybridization of recombinant lambda phage genomic libraries using cDNAs as hybridization probes. The A.alpha. gene is located at the 3' end of the gamma, gene and consists of 5 exons. Three single nucleotide differences Nucleotide sequences of the three genes coding for human fibrinogen Chung, Dominic W.; Harris, Jeff E.; Davie, Earl W. Dep. Biochem., Univ. Washington, Seattle, WA, 98195, USA Advances in Experimental Medicine and Biology (***1990***), 281 (Fibrinogen, Thromb., Coagulation, Fibrinolysis), 39-48 CODEN: AEMBAP; ISSN: 0065-2598 111 bib ab 80-92 FILE (FILE 'HOME' ENTERED AT 20:02:30 ON 22 JUN 2004) ANSWER 80 OF 92 CAPLUS COPYRIGHT 2004 ACS on STN The gene for the A.alpha. chain of human fibrinogen was isolated by plaque Journal; General Review 117:144541 992:544541 CAPLUS and py<=2000 92 L9 ANI 'REGISTRY' ENTERED AT 20:03:02 ON 22 JUN 2004 0 S C[PRNDQGESTW] [ANDQEGILMEPSTWYY] [EGKSY] [FDENQEGKSTW] [RGW] [LIKM 0 S CFOKGSTLC 0 S MKFCDGEPWLFCWDG 159 S C[PRQST] [ANDQEGILMEPSTWYV] [ES] [FDENQSTY] W[LIMNQSTV] [FWY]/SQSP 406 S L1/SQSP AND PY<=2000

AB This report presents the sequences of the Chlamydomonas reinhardtii and Arabidopsis thaliana tufA genes and mol. phylogenetic evidence for the transfer of the chloroplast tufA gene to the nucleus in the green algal ancestor of land plants. The tufA gene, encoding chloroplast protein synthesis elongation factor Tu (EF-Tu), was first identified as a chloroplast gene in C. reinhardtii by filter hybridization. In this report, the Arabidopsis tufA-hybridizing fragment was isolated from a genomic DWA library and sequenced together with the Chalmydomonas tufA. Both loci contain a single, uninterrupted open reading frame which are absent in clotteds at the 5' end of the Arabidopsis open reading frame which are absent in all other known eubacterial and chloroplast tufAs which seem to encode a typical chloroplast transit peptide. The rest of the Arabidopsis sequence similarity between the two genes is 7'% for the amino acids and 67% for nucleotides. Northern blotting was used to show that the Arabidopsis tufA gene is actively expressed as a single transcript of appxx.2 o kilobases (kb). The evolutionary relationship between the Arabidopsis muclear tufA and known chloroplast tufA genes was investigated by phylogenetic anal. using amino acids sequences of EF-Tu and EF-1.alpha., the evalution of chloroplast-encoded EF-Tus. This group is, in turn, the sister group to a clade cong, the EF-Tu of the cyanobacteria. Thus, the Arabidopsis nuclear tufA seems to be derived form. Baldauf, Sandra L.; Palmer, Jeffrey D.
Dep. Biol., Univ. Michigan, Ann Arbor, MI, 48109, USA
Nature (London, United Kingdom) (***1990***), 344
CODEN: NATURS; ISSN: 0028-0836 Evolutionary transfer of the chloroplast tufA gene to the nucleus from a green algal chloroplast gene.), 344(6263),

1881 Nucleotide sequence of the .alpha.-amylase gene (ALP1) in the yeast ANSWER 82 OF 92 CAPLUS COPYRIGHT 2004 ACS on STN 1987:630391 CAPLUS

SO So Saccharomycopsis fibuligera

Itoh, Tetsuya; Yamashita, Ichiro; Fikui, Sakuzo
Fac. Eng., Hiroshima Univ., Higashi-Hiroshima, 724, Japan
FEBS Letters (***1987***), 219(2), 339-42

CODEN: FEBLAL; ISSN: 0014-5793

8 E 9

ALP1 from the yeast S. fibuligera was detd. The ALP1 DNA hybridized to a polyadenylated RNA of 2.0 kilobases. A single open reading frame encodes a 494-amino acid protein which is highly homologous with .alpha.-amylase (Taka-amylase) of complete nucleotide sequence of the secretable .alpha.-amylase gene l from the yeast S. fibuligera was detd. The ALP1 DNA hybridized to a Aspergillus oryzae.

ANSWER 83 OF 92 CAPLUS COPYRIGHT 2004 ACS 9 STN

김물론

106:46266

determination of the determination of its amino acid sequence, reactive site, and preparation of all three

Ikunoshin; Schrode, James; Kohr, William J.; Laskowski, Michael, Larayette, IN, 47907, USA 26(1), 193-201

Dep. Chem., Purdue Univ., West Lafayette, Biochemistry (***1987***), 26(1), 193-CODEN: BICHAW; ISSN: 0006-2960

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AB The complete amino acid sequence of chicken ovomucoid (ONCHI) is presented. ONCHI consists of 3 tandem domains, each homologous to pancreatic secretory trypsin inhibitor (Kazal) and each with an actual or putarive reactive site for inhibition of serine proteinases. The major reactive site for bovine .beta.-trypsin is the Arg89-Ala90 peptide bond in the 2nd domain. The equil. const. for hydrolysis of this peptide bond, KOhyd, is 1.85. The 1st and 3rd domains of ONCHI are relatively ineffective inhibitors of several serine proteinases against which they were tested. ONCHI is a mixt. of 2 forms: the major form with all of the amino acid residues and a minor form with vall34-Seri15 deleted. This polymorphism is present in all chicken eggs and is the result of ambiguous excision at the 5' end of the F intron. Procedures are given for prepn. of modified chicken ovomocoid, ONCHI? (In which the Arg89-Ala90 bond is hydrolyzed), of the 1st domain, ONCHI1 (residues 1-68), of the 2nd domain ONCHI2 (residues 65-130), and of the 3rd domain, ONCHI3 (residues 1-75-1)-glycosylated form, ONCHI3(+), and the carbohydrate-free form, ONCHI3(-), were obtained. These isolated native domains are useful in many studies were obtained. These of ovomucoid behavior.

ANSWER 84 OF 92 CAPLUS COPYRIGHT 2004 ACS on STN 1986:438578 CAPLUS

05:38578

R R E One- and two-dimensional NMR spectral analysis of the consequences of R.; Ortiz-Polo,

single amino acid replacements in proteins Markley, John L.; Croll, David H.; Krishnamoorthi, R.; Ortiz-Polo, Gilberto, William M.; Bogard, W. C., Jr.; Laskowski, M., Gilberto, William M.; Bogard, W. C., Jr.; Laskowski, M., Dep. Biochem., Univ. Wisconsin, Madison, WI, 53706, USA Journal of Cellular Biochemistry (***1986***), 30(4), 291-309 CODEN: JCEBD5; ISSN: 0730-2312

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The set of avian ovomucoid third domains, which consists of the third domain proper plus a short leader (connecting peptide) and has a max of 56 amino acid residues, offers an attractive system for developing exptimethods for investigating sequence-structure and structure-function heteronuclear 2-dimensional NMR were used. relationships in proteins. NMR results provided examples of sequence effects on pKa' values, av. conformation, and internal motion of amino data were obsd. obsd. with single substitution variants. Agreement between x-ray and NMR acid side chains. One-dimensional, homonuclear 2-dimensional, and mensional NMR were used. Variations in NMR spectra were amino

ANSWER 85 OF 92 CAPLUS COPYRIGHT 2004 ACS on

BamHI F region of the B95-8 Epstein-Barr virus genome Bart G.

SO SO Hudson, Graham S.; Gibson, Toby J.; Barrell, MRC Lab. Mol. Biol., Cambridge, CB2 2QH, UK Virology (***1985***), 147(1), 99-109

CODEN: VIRLAX; ISSN: 0042-6822

AB FI

used to search for mRNAs. Four rightward-reading frames encoding basic proteins appear to be expressed by 3'-coterminal early mRNAs. Two The BamHI F region of the B95-8 Epstein-Barr virus (EBV) genome was sequenced and analyzed for transcription signals and open reading frame S1 mapping and northern blotting with probes from M13 recombinants was mKNAS. leftward-reading frames appear to be expressed by 31-coterminal early open reading frames.

11 8 8 11 ANSWER 86 OF 92 CAPIUS 1985:573275 CAPIUS COPYRIGHT 2004 ACS on STN

Evolution and structure of the fibrinogen genes. Random insertion of

βU introns or selective loss?
Crabtree, Gerald R.; Comeau, Claudette M.; Fowlkes, Dana M.; Fornace,

SO

Albert J., Jr.; Malley, James D.; Kant, Jeffrey A.
Med. Sch., Stanford Univ., Stanford, CA, 94305, USA
Journal of Molecular Biology (***1985***), 185(1), 1-19
CODEN: JMCBAK; ISSN: 0022-2836

Journal

853

Chromosomal linkage as well as sequence homologies provide unequivocal evidence that the genes for the alpha, beta and gamma chains of fibringen arcse by successive duplication of a single ancestral gene yet, when the 3 fibringen chains are aligned by amino acid homol, the positions of intervening coincide at only 2 positions for all 3 chains. Whereas 1 addnl. intron occurs at a homologous site in the beta and gamma. chains, none of the positions of the remaining 11 introns in the 3 genes is shared. This arrangement of introns in the 3 fibringen genes suggests that either introns were selectively lost, implying that there is essential information in the retained introns, or the common introns were present in the ancestral fibrinogen gene and introns have been randomly inserted since the triplication of the original gene. The more likely possibility of selective loss of introns implies that the ancestral gene, as it existed apprail billion years ago, must have been composed of numerous small exons.

ANSWER 87 OF 92 CAPLUS COPYRIGHT 2004 ACS on STN

983:517030 CAPLUS

1881 Partial mRNA sequences for human A.alpha., B.beta., and .gamma. fibrinogen

SO chains: Evolutionary and functional implications Kant, Jeffrey A.; Lord, Susan T.; Crabtree, Gerald R. Lab. Pathol., Natl. Cancer Inst., Bethesda, MD, 20205, USA Proceedings of the National Academy of Sciences of the United States America (**1983***), 80(13), 3953-7

CODEN: PNASA6; ISSN: 0027-8424

853

Rat cDNA and genomic probes were used to screen a human liver cDNA library to isolate clones of 2274, 855, and 736 base pairs (bp) coding for the A.alpha. B.beta., and .gamma. chains of human fibrinogen. Sequence anal. reveals a hitherto unrecognized extension of 15 amino acids at the C-terminus of the A.alpha. chain, the terminal residue of which is proline. This brings the known length of the human A.alpha. chain chain to 625

> B.beta. and gamma. chain coding regions confirms that these genes have arisen by duplication and subsequent divergence of an ancestral gene. A comparison of human and rat. gamma. chain cDNAs shows >88% sequence homel over the C-terminal 162 amino acids, implying strong selective pressures amino acids. The 13-amino acid repeated region in the midportion of the A.alpha. chain clearly has arisen through an 8-fold duplication of a 39-bp genetic element, which itself appears to have been constructed from smaller 6-bp repeating units. Greater than 50% sequence homol. between on these portions of the .gamma. chain gene.

ANSWER 88 OF 92 CAPLUS COPYRIGHT 2004 ACS on STN CAPLUS

1983:417447 99:17447

12851

Characterization of a complementary deoxyribonucleic acid coding for the alpha. chain of human fibringen Rixon, Mark W.; Chan, Wai Yee; Davie, Earl W.; Chung, Dominic W. Dep. Biochem., Univ. Washington, Seattle, WA, 98195, USA Biochemistry (***1983***), 22(13), 3237-44

CODEN: BICHAW; ISSN: 0006-2960

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contained 2224 base pairs, including a noncoding region at the 5' end that was followed by a region coding for a signal peptide of 19 (or 16) amino acids and a mature protein of 625 amino acids, a stop codon of TAG, another noncoding region, and a poly(A) tail at the 3' end. Eight tandem repeats of 39 base pairs were obed. Which started with nucleotide 905 (amino acid residue 270) and ended with nucleotide 1213 (amino acid residue 270) and ended with nucleotide 1213 (amino acid residue 372). The identity in the nucleotide sequence in the tandem repeats ranged 72-95% when compared to a consensus sequence. The predicted amino acid sequence for the mature polypeptide chain was 15 amino acids longer at the C-reminal end than that of the alpha. chain isolated from plasma fibrinogen and sequenced. Apparently, minor proteolysis of the C-terminus of the alpha. Chain is a chain and that contains the contract of the compared to a consensus sequence of the alpha. hybridization probe. Several human clones coding for the alpha. chain were identified, and 1 of these was used to rescreen the entire cDNA library of 18,000 recombinants. Plasmids with the largest cDNAs were A human liver cDNA library was screened for the .alpha. chain of fibrinogen with a cDNA clone from the corresponding bovine mol. as a during secretion or circulation of the protein in plasma. isolated, and their inserts were sequenced. The largest cDNA insert

ANSWER 89 OF 92 CAPLUS COPYRIGHT 2004 ACS on STN CAPLUS

.981:116302

94:116302

SO SO Human fibrinogen: sequence, sulfur bridges, glycosylation and structural variants some

Henschen, A.; Lottspeich, F.; Southan, C.; Toepfer-Petersen, E. Max-Planck-Inst. Blochem., Martinsried, D-8033, Fed. Rep. Ger. Protides of the Biological Fluids (***1980***), 28th, 51-6 CODEN: PBFPA6; ISSN: 0079-7065

853

Human fibrinogen has the overall structure (A.alpha.,B.beta.,.gamma.)2. The complete amino acid sequences of the 3 chains with 610, 461, and 41: residues have been elucidated. The chains are held together by 29 SS bonds, 3 of which link the half-mols. to each other. Carbohydrate side chains are present in the B.beta.— and .gamma.—chains. Variants of the 411

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.gamma.-chain with considerably lower mol. wt. seem to be present in all individuals. The structural error in a new abnormal variant, fibrinogen Muenchen, has recently been identified as an Arg .fwdarw. Asn exchange in position 3 of the .alpha.-chain.

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TRAE
Primary sequence of ovomucoid messenger RNA as determined from cloned
                                              ANSWER 90 OF 92 CAPLUS
                                1981:42807
                                                COPYRIGHT 2004 ACS on
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SO Ã Dep. Cell Biol., Baylor Coll. Med., Houston, TX, 77030, USA Journal of Cell Biology (***1980***), 87(2, Pt. 1.), 480-7 CODEN: JCLBA3; ISSN: 0021-9525 Catterall, James F.; Stein, Joseph P.; Kristo, Paula; Means, Anthony R.; O'Malley, Bert W. complementary DNA

AB EST

AB COMMICCIA MANA (MANAMA) COMPILIES - GAPIA OF THE COURT MANA (MANAMA) COMPILIES - GAPIA OF THE COUNTY OF THE COURT OF THE COMPILIANT DIAMENTAL PORTION CONTRIBUTED OF THE COMPILIANT DIAMENTAL PROPERTY TO THE 5' end of MRNAOM WAS Obtained from a partially purified preprior of MRNAOM by Polymn. by reverse transcriptase in the presence of a restriction fragment primer from poMI(0). The complementary DNA mixt, was amplified by mol. cloning using poly(dG)/poly(dC) tailing to form recombinant bacterial plasmids. Recombinant plasmids contg. overmood DNA sequences were selected by in situ hybridization to 32P-labeled poMI(0) fragments. The longest plasmid contg. overmood DNA sequences were selected by in sequence of both poMI(0) and poMI(0) fragments. The longest plasmid contg. overmood DNA sequences was designated poM502. The complete DNA sequence of both poMI(0) and poM502 was detd. The 2 plasmids appear to contain sequences complementary to the entire length of mRNAOM. The nucleic acid sequence agrees with the known amino acid sequences for both overminal signal peptide. Highly homologous sequences occur in 2 regions that coincide with structural domains of the protein: Comparison of the sequence of mRNAOM with that for other eukaryotic mRNAs allowed identification of possible functional regions in the mRNA mol. Ovomucoid mRNA (mRNAom) comprises .apprx.8% of the total mRNA in the

ANSWER 91 OF 92 .980:17417 CAPIUS CAPLUS COPYRIGHT 2004 ACS on STN

92:17417

SER SE The amino acid sequence of the .alpha.-chain of human fibrinogen Doolittle, R. F.; Watt, K. W. K.; Cottrell, B. A.; Strong, D. D.; Riley,

SOS Dep. Chem., Univ. California, San Diego, CA, 92093, USA Nature (London, United Kingdom) (***1979***), 280(5722), 464-8 CODEN: NATUAS; ISSN: 0028-0836

AB F3 Journal

amino-terminal third, zones of apprx.200 residues, each of unique amino acid compn. The regions were designated ZN, ZM, and ZC and corresponded roughly to the sites The structure of human fibrinogen .alpha.-chain could be divided terminal third, the middle third, and the carboxy-terminal third, 2M contained the 2 primary .alpha.-chain crosslinking acceptor and consisted of a series of internal duplications.

ANSWER 92 OF 92 1980:1856 CAPLU CAPIJUS COPYRIGHT 2004 ACS on STN

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Amino acid sequence studies on the .alpha. chain of human fibrinogen.

AB The complete amino acid sequence of the .alpha. chain of human fibrinogen AB The complete amino acid sequence of the .alpha. chain of human fibrinogen of 66,125. The chain has 10 methionines, and fragmentation with CNBr yielded 11 peptides. The arrangement of the 11 fragments was detd. by the isolation of peptide overlaps from plasmic and staphylococcal protease digests of fibrinogen and(or) .alpha. chains. In addn., certain of the CNBr fragments, preliminary reports of whose sequences have appeared previously, were reexamd. to resolve several discrepancies. The .alpha. chain is homologous with the .beta. and .gamma. chains of fibrinogen, although a large repetitive segment of unusual compn. is absent from the latter 2 chains. The existence of this unusual segment divides the sequence of the .alpha. chain into 3 zones of .apprx.200 residues each that are readily distinguishable on the basis of amino acid compn. alone. Overlapping sequences providing the complete sequence Watt, K. W. K.; Cottrell, B. A.; Strong, D. D.; Doolittle, R. F. Dep. Chem., Univ. California, La Jolla, CA, 92093, USA Biochemistry (***1979***), 18(24), 5410-16 CODEN: BICHAW; ISSN: 0006-2960

853

SO SO

=> d 14 sqd 100 YOU HAVE REQUESTED DATA FROM FILE 'REGISTRY' - CONTINUE? (Y)/N:y

FS SQL NTE SEQ terminal mod. modified ANSWER 100 OF 159 RE-442513-71-5 REGISTRY 19 PROTEIN SEQUENCE; STEREOSEARCH Trp-1 Lys-19 ----- location -----REGISTRY 1 4 COPYRIGHT 2004 ACS N-acetyl C-terminal amide description 9 STN

1 WAPCQEEPWL FCFHGGGGK

SIIH AT: 4-11

=> d 14 sqd 1-5 YOU HAVE REQUESTED DATA FROM FILE 'REGISTRY' - CONTINUE? (Y)/N:Y

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1 MTAWILLPVS LSAFSITGIW TVYAMAVMNR HVCPVENWSY NDSCSPDPAE

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51 QGGPKTCCTL DDVPLISKCG TYPPESCLFS LIGNMGAFMV ALICLLRYGQ

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                                                                                                                                                                                                                                                                                                                                                                                                            ANSWER 3 OF 159 REGISTRY COPYRIGHT 2004 ACS on STN 681717-61-3 REGISTRY PROTEIN SEQUENCE 289
                                                                                                                                                                         ANSWER 4 OF 159 REGISTRY COPYRIGHT 2004 ACS on STN 677365-49-0 REGISTRY
                                                                                                                                                      PROTEIN SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKEILLWALL NLIVALAFNE DYTVSSTEPY LVYLKSDYLE CAGVLIHELW
51 VITAAHCNLE KLRVILGVTI PADSNEKHLQ VIGYEKMIHH PHESVTSIDH
101 DINLIKLKTE AELNDYVKLA NLEYQTISEN TKCSVSTWSY NVCDIYKEPD
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151 HIOLLGKUVR AQLVIDKRILE VDIDIKIRSC RGSCSBALAR EVDLKDYEDQ
201 QKOLEQVIAK DLLPVNLOV TANLLVARV ITEETPHLA RAIKWQYRFE
251 VKPINKEHIA PREAMINIAL SEVSTILLIWG SLPCFPRLS
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201 CNGMLQGILS FADGCVLRAD VGIYAKIFYY IPWIENVIQN N
1: 133-140
                                                                                                                                                                                                                                                                                                                                                   1 MESMRIVCLV LSVVGTAWTA DSGEGDFLAE GGGVRGPRVV ERHQSACKDS
51 DWPFCSDEDW NYKCPSGCRM KGLIDEVNQD FTNRINKLKN SLFEYQKNNK
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|SEQID 1514

101 LLEQNRHSWI NTTALITGCT NAAGLVAVGN FQVDHAKSIH YIGAGVAFPA
151 GLLEVGLKGV LEYHGATTPL DMAMAYLBSV LAVIAFVTLV LSGVFFIHES
201 SELQHGAALC EWVFVLDILI EYGTFSYEFG AVSSDTLVAA LQPAPGRACK
251 SSGSSSTSTH LNCAPESIAN I
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RELATED SEQUENCES AVAILABLE WITH SEQLINK

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4242736 A1 19940623 DE 1992-4242736 199212 605797 A1 19940713 EP 1993-119574 199312 605797 B1 19990317 EP 1997	CODEN: GWXXBX Patent German CNT 1 PATENT NO. PATENT NO.	ANSWER 1 OF 1 CAPIUS COPYRIGHT 2004 ACS on STN 1994:506510 CAPIUS 121:106510 Synthetic peptides from fibrinogen and anti-peptide antibodies for use in immunoassay and treatment of fibrinolytic disorders Kraus, Michael; Stueber, Werner Behringwerke AG, Germany Ger. Offen., 34 pp.	s 112 not 110 1 L12 NOT L10 d 113 bib ab	s 111 ar	FILE 'BIOSIS, CAPLUS' ENTERED AT 20:41:34 ON 22 JUN 2004 FILE 'BIOSIS, CAPLUS' ENTERED AT 20:41:35 ON 22 JUN 2004	'REGISTRY' ENTERED AT 20:40:23 ON 22 JUN 2004	FILE 'BIOSIS, CAPLUS' ENTERED AT 20:33:24 ON 22 JUN 2004 103 S L4 217 S L5 296 S L6 OR L7 249 DUP REM L8 (47 DUPLICATES REMOVED) 2 S L9 AND FIBRIN (W) BIND? 92 S L9 AND PY<=2000	FILE 'REGISTRY' ENTERED AT 20:03:02 ON 22 JUN 2004 0 S C(PRNDQGFSTW)[ANDQEGILMFPSTWYV][EGKSY][PDENQEGKSTW][RGW][LIKM 0 S CFOKGGTLC 0 S WKFCDGEPWLFCWDG 159 S C(PRNGST][ANDQEGILMFPSTWYV][ES][PDENQSTY]W[LIMNQSTV][FWY]/SQSP 406 S L1/SQSP

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US 1996-727045 A3 19961008
A method is described for obtaining synthetic peptides by plasmin cleavage of fibringen to yield C-terminal ends of the E fragment which are also antigenic. The peptides are injected into rabbits to produce antibody-producing cells which are used to generate monoclonal antibodies for use in immunoassays or in the treatment of fibrinolytic disorders.

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=> s W[AQEKM][ALMP]CP[DEGMW]E(NDEPS]W[LT]FCW[DGHFS][AGHPS]/sqsp

5 W[AQEKM][ALMP]CP[DEGMW]E[NDEPS]W[LT]FCW[DGHFS][AGHPS]/SQSP

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> DT Patent LA English FAN.CNT 1 LA English FAN.CNT 1 PRAI OS AB DN TII ΡI ΑB PRAI US 2002-360851P US 2003-440411P The present invention relates to polypeptides useful for detecting and targeting primary receptors on endothelial cells for VEGF, i.e., VEGF receptor 2, also known as kinase domain region (KDR) and feat liver kinase-1 (Flk-1), and for imaging and targeting complexes formed by VEGF and KDR. The involvement of VEGF and KDR in anglogenesis makes the VEGF/KDR and KDR binding polypeptides of the present invention particularly useful for imaging important sites of angiogenesis, e.g., recolastic tumors, for targeting substances, e.g., therapeutics, including radiotherapeutics, to such sites, and for treating certain disease states, including those assocd, with inappropriate angiogenesis. Disclosed are synthetic, isolated polypeptides capable of binding KDR or VEGF/KDR complax with high affinity (c. a. having a KTK) mr. M.) WO 2003074005 W: AE, A US 2003143158 US 2001-34974 MARPAT 139:138721 ANSWER 2 OF 3 CAPLUS 2003:590577 CAPLUS PATENT NO. PATENT NO. U.S. Pat. Appl. Publ., 41 pp. Fibrin binding moieties useful as imaging agents Wescott, Charles R.; Beltzer, James P.; Sato, Aaron K. complex with high affinity (e.g., having a KD<1 .mu.M). CODEN: USXXCO 39:138721 AG, AL, AM, CZ, CZ, LU, LU, LU, LV, LV, VS, UZ, VS, UZ, CZ, DE, CZ KIND 2 KIND Δ1 , MW, MZ, , DK, EE, , SI, SK, , SN, TD, 20020301 20030912 , AT, AU, , DE, DK, COPYRIGHT 2004 ACS on STN DATE 20030731 DATE 20030115 VC, S S S SD ES TR YU, SE, DM, AZ, 87. 138 SG, AK WO 2003-US6731
> BA, BB, BG, BR, B
> DZ, EC, EE, ES, F
> JP, KE, KG, KP, K
> MK, MN, MM, MX, M
> SG, SK, SL, TJ, T
> ZA, ZM, ZM, AM, A APPLICATION NO. US 2001-34974 APPLICATION NO. FR, BJ, 997 ç , ç MZ, MZ, , i j DATE DATE 20011221 20030303 BY NO SB BZ A E A GA, KG R CA 8 F B KZ T O K E C 88 844489

The present invention provides binding moieties for fibrin which have a variety of uses wherever detecting, isolating or localizing fibrin, and particularly fibrin as opposed to fibringen, is advantageous. Particularly disclosed are synthetic, isolated polypetides capable of binding fibrin and recognizing the form of polynd. Fibrin found in thrombi. In addn., the polypeptides have a slow dissoon, rate from fibrin, which improves their ability to form a contrast image at the site of a fibrin clot, making the disclosed binding moieties particularly useful as imaging agents for thrombi.

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variety of uses wherever detecting, isolating or localizing fibrin, and particularly fibrin as opposed to fibrinogen, is advantageous. Particularly disclosed are synthetic, isolated polypeptides capable of binding fibrin and recognizing the form of polymod. Fibrin found in thrombi. In addn., the polypeptides have a slow dissoon, rate from fibrin, which improves their ability to form a contrast image at the site of a fibrin clot, making the disclosed binding moieties particularly useful as imaging agents for thrombi. Among examples provided are: screening of phage display libraries using the sol. fibrin-derived polypeptide DD(E) as fibrin target, and scintigraphic imaging of clots in WO 2001-US49534 MARPAT 137:90279 WO 2002055544 WO 2002055544 Fibrin binding moieties useful as imaging agents Wescott, Charles R.; Beltzer, James P.; Sato, Aaron K. PATENT NO. English Dyax Corp., USA MARPAT 177:902/9
The present invention provides binding moieties for fibrin which have a CODEN: PIXXD2 Int. 4,6,4,6,4 KIND & & 286188 DATE 20020718 20030327 AT, AU, DE, DK, IL, IN, MA, MD, SD, SE, VN, YU, ξĘ, & 8 8 DM, IS, IS, SG, SG, SL, SZ, GR, IE, GN, GQ, EP 20 DZ, JP, SI, ZM, ŏ APPLICATION NO. SK ME BB 2001-US49534 W, TI, MW, SL, ¥ £ 2 MX, ES, ĽU, ₹, 6, 24 DATE 20011221 K I O K B BZ KE NE CO SN, MC, E SE 222599 염쓸

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AN DN TI Fibrin binding moieties useful as imaging agents Wescott, Charles R.; Beltzer, James P.; Sato, Aaron K. 39:138721

US 200318022 Ai 20030925

US 2002-209183 20020730

PRAI US 2003-209721P P 20010730

AB The invention is based on peptides and peptide-targeted multimeric contrast agents for MR, optical, and radionuclide imaging, in which a single peptide can function both as a targeting group and a point of attachment for one or more chelates at both the N- and C-termini, either directly or via an optional intervening linker. Contrast agents can have the formula (chelate)-1-0-(linker)-0-5-(linker-submit)0-1]-[NRACHRICO]n, where R1 is an amino acid side chain or deriv. and R2 is H or an aliph. group. Contrast agents of the invention maintain binding affinity for biol. targets such as fibrin and high relaxivity. Thus, peptide
H-Leu-Pro-Cys-Asp-Tyr-Tyr-Gly-Thr-Cys-Bip-Asp-NHCH2C6H4CH2NH2-m (Bip =

U.S. Pat: Appl. Publ., 41 pp. CODEN: USXXCO

RW: GH, GN, KE, LS, MM, MZ, SI
CY, DE, DK, ES, FI, FR, GI
BF, BJ, CF, CG, CI, CM, GB
EP 1348026 A2 20031001
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WO 2001-US45534 W 20011221 DT Pate LA Engl FAN.CNT 1 SO DN TH Ä => d 119 bib ab 1-5 ANSWER 1 OF 5 CAPLUS rabbits using 99mTc-labeled peptides. COPYRIGHT 2004 ACS 8

PI US 2003143158 *I*PRAI US 2001-34974
OS MARPAT 139:138721
AB The present inventi HI HA EI LA English FAN.CNT 1 A E B SO Ag English variety of uses wherever detecting, isolating or localizing fibrin, and particularly fibrin as opposed to fibrinogen, is advantageous. Particularly disclosed are synthetic, isolated polypeptides capable of binding fibrin and recognizing the form of polymd. Fibrin found in thrombi. In addn., the polypeptides have a slow dissoon, rate from fibrin, which improves their ability to form a contrast image at the of a fibrin clot, making the disclosed binding moieties particularly useful as imaging agents for thrombi. Epix Medical, Inc., USA PCT Int. Appl., 177 pp. CODEN: PIXXD2 Preparation of peptide-based multimeric targeted contrast agents Prang, Zhaoda; Caravan, Peter D.; McMurry, Thomas J.; Kolodziej, Andri Shrikumar; Amedio, John C.; Dumas, Stephane; Wang, Xifang; Sun, Wei-Chuan; Nivorozhkin, Alexander L.; Koerner, Steffi K. ANSWER 2 OF 5 The present invention provides binding moieties for fibrin which have a PATENT NO. WO 2003011115 W: AE, AG, AL,
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biphenylalanyl) was prepd. and applied to the synthesis of contrast agent (Gd-DTPA-CONHCH2CH2)2NCH2CO-peptide disulfide-COCH2N(CH2CH2NHCO-DTPA-Gd)2.

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Particularly disclosed are synthetic, isolated polypeptides capable of binding fibrin and recognizing the form of polyme. Fibrin found in thrombi. In addn., the polypeptides have a slow dissoon, rate from fibrin, which improves their ability to form a contrast image at the site of a fibrin clot, making the disclosed binding moieties particularly useful as imaging agents for thrombi. Among examples provided are: screening of phage display libraries using the sol. fibrin-derived polypeptide DD(E) as fibrin target, and scintigraphic imaging of clots in rabbits using 99mTc-labeled peptides.
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In particular, this invention relates to novel multimeric compose which exhibit improved relaxivity properties upon binding to endogenous proteins or other physiol. relevant sites. The compds. consist of: a) two or more Image Enhancing Moieties (IEMs) (or signal-generating moiety) comprising multiple subunits; b) two or more Target Binding Moieties (TBMs), providing for in vivo localization and multimer rigidification; c) a scaffold framework for attachment of the above moieties; and d) optional linkers for attachment of the IEMs to scaffold. This invention also relates to pharmaceutical compns. comprising these compds. and to methods of using the compds. and compns. for contrast enhancement of diagnostic FP BR 2000013171 1210124 AT, BE, IE, SI, 성 년 SI, çç, 두 유 CI, ₹ % ۲, E 9,3 20020528 20020605 DK, ES, FI, RO, ₩. ₩. ₽, %, GB, GR, IT, L1, LU %, CY, AL JP 2001-513442 JP 2002-341392 US 2000-627719 ZA 2002-624 NO 2002-474 US 2003-445544 , IE, IT, LU, MC, NI , ML, MR, NE, SN, TI BR 2000-13171 EP 2000-950815 ĽU, TD, 20000728 20000728 PT, SE, NL, SE, MC, ₽, P BJ,

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IN TO A LZO 멀 FAN DE SO 2 WO 2003074005 KDR and VEGF/KDR binding peptides and their use in diagnosis and therapy Sato, Aaron K.; Sexton, Daniel J.; Ladner, Robert C.; Dransfield, Daniel T.; Swenson, Rolf E.; Marinelli, Edmund R.; Ramalingam, Kondareddiar; Nunn, Adrian D.; Von Wronski, Mathew A.; Shrivastava, Ajay; Pochon, Sibylle; Bussat, Philippe; Arbogast, Christophe; Pillai, Radhakrishna; Fan, Hong; Linder, Karen E.; Song, Bo; Nanjappan, Palaniappa pyak Corp., USA; Bracco International B.V.; et al. ANSWER 1 OF 3 CAPIL 2003:719271 CAPILUS PATENT NO. English Patent CODEN: PIXXD2 39:265740 Int. ε, 2,52,88£ Appl., HR, CR, CAPIUS COPYRIGHT 2004 ACS on STN 585555 350 pp. KIND ₹ ξ, ξ, 20030912 VC, SC, VC, SO, SO, SO, DZ, SG, ZA, š APPLICATION NO. ZK, WS, EC, BB, 2003-US6731 BR, ES, KP, AM, MZ, BΥ, 20030303 , BZ, CA, , GB, GD, , KZ, LC, , NO, NZ, , NO, NZ, , HY, KG, DATE 218489 822529 922529

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Fibrin binding moieties useful as imaging agents Wescott, Charles R.; Beltzer, James P.; Sato, Aaron K. Dyax Corp., USA

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Patent

PCT Int. Appl., 89 pp. CODEN: PIXXD2

English

PRAI ΑB neoplastic tumors, for targeting substances, e.g., therepoutics, including radiotherapoutics, to such sites, and for treating certain disease states, including those assocd. With inappropriate angiogenesis. Disclosed are synthetic, isolated polypeptides capable of binding KOR or VEGF/KDR complex with high affinity (e.g., having a KDK1 .mu.M). targeting primary receptors on endothelial cells for VEGF, i.e., VEGF receptor 2, also known as kinase domain region (KDR) and fetal liver kinase-1 (Flk-1), and for imaging and targeting complexes formed by VEGF and KDR. The involvement of VEGF and KDR in angiogenesis makes the VEGF/KDR and KDR binding polypeptides of the present invention particularly useful for imaging important sites of angiogenesis, e. g., US 2002-360851P US 2003-440411P The present invention relates to polypeptides useful for detecting Σ. 88888 18914 M B C E H SE, DE DK, EE, SI, SK, SN, TD, 20020301 20030115 TG SD, SI, SZ, FR, G 8 2 ୧୯,୯୭ CI, HU, ZM, MZ E X AT, 8 E E 8988

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STRUCTURE FILE UPDATES: 21 JUN 2004 HIGHEST RN 697224-75-2 DICTIONARY FILE UPDATES: 21 JUN 2004 HIGHEST RN 697224-75-2

TSCA INFORMATION NOW CURRENT THROUGH JANUARY 6, 2004

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Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the wab at: http://www.cas.org/ONLINE/DBSS/registryss.html

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PI PRAI OS AB PA III AN DN TI IN PA SO とは => s (130 or 134) and fibrin L35 3 (L30 OR L34) J L34 L33FAN. ONT => d 135 bib ab 1-3 English .CNT 1 US 2003143158 US 2001-34974 MARPAT 139:138721 FILE Dyax Corp., USA PCT Int. Appl., 89 pp. CODEN: PIXXD2 ***Fibrin*** binding moieties useful as imaging agents Wescott, Charles R.; Beltzer, James P.; Sato, Aaron K. isolated polypeptides capable of binding the form of polymd. ***fibrin*** foun polypeptides have a slow dissocn. rate from ***fibrin*** , and particularly ***fibrin*** as opposed to fibrinogen, is advantageous. Particularly disclosed are synthetic, isolated polypeptides capable of binding ***fibrin*** and recognitions. have a variety of uses wherever detecting, isolating or localizing ***fibrin*** as opposed to ***Fibrin*** binding moieties useful as imaging agents Wescott, Charles R.; Beltzer, James P.; Sato, Aaron K. ANSWER 1 OF 3 CAPLUS 2003:590577 CAPLUS FILE 'BIOSIS, CAPLUS' ENTERED AT 21:59:05 ON 22 JUN 2004 $1479\ \text{S}\ \text{L}33$ PATENT NO. Patent ANSWER 2 OF 3 CAPLUS The present invention provides binding moieties for PATENT NO. English FILE 'BIOSIS, CAPLUS' ENTERED AT 21:57:25 ON 22 JUN 2002:539700 improves their ability to form a contrast image at the site of a
fibrin clot, making the disclosed binding moieties particularly
useful as imaging agents for thrombi. Patent 137:90279 CODEN: USXXCO 139:138721 .S. Pat. Appl. Publ., 41 pp. 'REGISTRY' ENTERED AT 21:57:41 ON 22 JUN 2004 3623 S C.{2}[EGKSY].{1}[RGW].{1}[ILFWY]C/SQSP CAPLUS KIND KIND 2 20030731 COPYRIGHT DATE DATE COPYRIGHT 2004 ACS on SIN AND FIBRIN 2004 found in thrombi. In addn., the from ***fibrin*** , which ACS S APPLICATION NO. APPLICATION NO. 2001-34974 9 2004 ***fibrin*** DATE DATE 20011221 and recognizing which

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                                                                                                                                                                    Synthetic peptides from fibrinogen and anti-peptide antibodies for use in immunoassay and treatment of fibrinolytic disorders Kraus, Michael; Stueber, Werner
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